

## SEARCH NOTES

09 DEC 02

**09/833,790**

Databases searched: USPATFULL via EAST, EUROPATFULL via EAST, CAplus, and Medline

Reviewed parent application(s): see the Bib data sheet

### **Search terms:**

Inventor(s) : e.g. Lodes M?/au

The STIC performed a search of SEQ ID NO: 365.

309

**SEQ ID NO: 365**

RESULT 4

AAA97368

ID AAA97368 standard; cDNA; 5277 BP.

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AC AAA97368;

XX

DT 29-JAN-2001 (first entry)

XX

DE Human colorectal cancer modulator protein BCN5 cDNA.

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KW Colorectal cancer modulator protein; CCMP; human; expression profile;

KW drug screening; diagnosis; prognosis; antibody; vaccine; BCN5;

KW immunogenic; gene therapy; targetting moiety; CCMP inhibitor; tumour; ss.

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OS Homo sapiens.

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PN WO200055633-A2.

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PD 21-SEP-2000.

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PF 15-MAR-2000; 2000WO-US0704.

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PR 15-MAR-1999; 99US-0268866.

PR 09-NOV-1999; 99US-0435945.

PR 09-NOV-1999; 99US-0436983.

PR 29-NOV-1999; 99US-0450857.

PR 02-DEC-1999; 99US-0453850.

PR 28-JAN-2000; 2000US-0493444.

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PA (EOSB-) EOS BIOTECHNOLOGY INC.

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PI Mack D, Gish KC, Wilson KE;

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DR WPI; 2000-638217/61.

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PT Use of expression profiles, nucleic acids and proteins involved in  
PT colorectal cancer for diagnosis and prognosis of colorectal cancer and  
PT identifying candidate agent and/or targets which modulate colorectal  
PT cancer -

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PS Claim 1; Fig 45; 308pp; English.

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CC The invention relates to the use of expression profile nucleic acids  
CC encoding colorectal cancer modulator proteins (CCMPs) for screening  
CC drug candidates and bioactive agents capable of binding and/or  
CC modulating CCMPs; for evaluating the effect of drugs for the treatment of  
CC colorectal cancer; for the diagnosis and prognosis of colorectal cancer;  
CC and as a target for colorectal cancer therapy. The expression profile  
CC nucleic acids used in the methods of the invention encode the CCMPs CZA8,  
CC BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CAA2,  
CC CAA9 and CGA8. The CCMPs (especially CJA8 (AAB23166)) may be used in  
CC vaccine compositions, and also to raise antibodies for use as therapeutic  
CC agents, or targetting moieties for therapeutic agents in the treatment  
CC of colorectal cancer. Inhibitors of CCMP activity may also be used in  
CC the treatment of other tumours. CCMP nucleotides, especially those  
CC encoding CJA8, may be used in gene therapy, and in genetic vaccines.  
CC Sequences AAA97355-A97371 represent nucleic acid sequences encoding a  
CC variety of colorectal cancer modulator proteins.

SQ Sequence 5277 BP; 1652 A; 1088 C; 1133 G; 1399 T; 5 other;

Query Match 99.9%; Score 4830.4; DB 21; Length 5277;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 4828; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GATGTGGAGCTGGGGTCCCTGCAAGTCATGAACAAAACGAGAAAGATTATGGAACATGGG 60
      |||
Db     416 GATGTGGAGCTCGGGTCCCTGCAAGTCATGAACAAAACGAGAAAGATTATGGAACATGGG 475

QY     61 GGGGCCACCTTCATCAATGCCTTTGTGACTACACCCATGTGCTGCCCCTCACGGTCTCTCC 120
      |||
Db     476 GGGGCCACCTTCATCAATGCCTTTGTGACTACACCCATGTGCTGCCCCTCACGGTCTCTCC 535

QY    121 ATGCTCACCGGGAAGTATGTGCACAATCACAATGTCTACACCAACAACGAGAACTGCTCT 180
      |||
Db     536 ATGCTCACCGGGAAGTATGTGCACAATCACAATGTCTACACCAACAACGAGAACTGCTCT 595

QY    181 TCCCCCTCGTGGCAGGCCATGCATGAGCCTCGGACTTTTGCTGTATATCTTAACAACACT 240
      |||
Db     596 TCCCCCTCGTGGCAGGCCATGCATGAGCCTCGGACTTTTGCTGTATATCTTAACAACACT 655

QY    241 GGCTACAGAACAGCCTTTTTTTGGAAAATACCTCAATGAATATAATGGCAGCTACATCCCC 300
      |||
Db     656 GGCTACAGAACAGCCTTTTTTTGGAAAATACCTCAATGAATATAATGGCAGCTACATCCCC 715

QY    301 CCTGGGTGGCGAGAATGGCTTGGATTAATCAAGAATTCTCGCTTCTATAATTACACTGTT 360
      |||
Db     716 CCTGGGTGGCGAGAATGGCTTGGATTAATCAAGAATTCTCGCTTCTATAATTACACTGTT 775

QY    361 TGTCGCAATGGCATCAAAGAAAAGCATGGATTTGATTATGCAAAGGACTACTTCACAGAC 420
      |||
Db     776 TGTCGCAATGGCATCAAAGAAAAGCATGGATTTGATTATGCAAAGGACTACTTCACAGAC 835

QY    421 TTAATCACTAACGAGAGCATTAATTACTTCAAAATGTCTAAGAGAATGTATCCCCATAGG 480
      |||
Db     836 TTAATCACTAACGAGAGCATTAATTACTTCAAAATGTCTAAGAGAATGTATCCCCATAGG 895

QY    481 CCCGTTATGATGGTGATCAGCCACGCTGCGCCCCACGGCCCCGAGGACTCAGCCCCACAG 540
      |||
Db     896 CCCGTTATGATGGTGATCAGCCACGCTGCGCCCCACGGCCCCGAGGACTCAGCCCCACAG 955

QY    541 TTTTCTAAACTGTACCCCAATGCTTCCCAACACATAACTCCAGTTATAACTATGCACCA 600
      |||
Db     956 TTTTCTAAACTGTACCCCAATGCTTCCCAACACATAACTCCTAGTTATAACTATGCACCA 1015

QY    601 AATATGGATAAAACACTGGATTATGCAGTACACAGGACCAATGCTGCCCATCCACATGGAA 660
      |||
Db    1016 AATATGGATAAAACACTGGATTATGCAGTACACAGGACCAATGCTGCCCATCCACATGGAA 1075

QY    661 TTTACAAACATTCTACAGCGCAAAGGCTCCAGACTTTGATGTGAGTGGATGATTCTGTG 720
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Db    1076 TTTACAAACATTCTACAGCGCAAAGGCTCCAGACTTTGATGTGAGTGGATGATTCTGTG 1135

QY    721 GAGAGGCTGTATAACATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTTAC 780
      |||
Db    1136 GAGAGGCTGTATAACATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTTAC 1195

QY    781 ACCGCCGACCATGGTTACCATATTGGGCAGTTTGGACTGGTCAAGGGGAAATCCATGCCA 840
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Db    1196 ACCGCCGACCATGGTTACCATATTGGGCAGTTTGGACTGGTCAAGGGGAAATCCATGCCA 1255
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Qy	841	TATGACTTTGATATTCGTGTGCCTTTTTTTATTCGTGGTCCAAGTGTAGAACCAGGATCA	900
Db	1256	TATGACTTTGATATTCGTGTGCCTTTTTTTATTCGTGGTCCAAGTGTAGAACCAGGATCA	1315
Qy	901	ATAGTCCACAGATCGTTCTCAACATTGACTTGGCCCCACGATCCTGGATATTGCTGGG	960
Db	1316	ATAGTCCACAGATCGTTCTCAACATTGACTTGGCCCCACGATCCTGGATATTGCTGGG	1375
Qy	961	CTCGACACACCTCCTGATGTGGACGGCAAGTCTGTCTCAAACCTTCTGGACCCAGAAAAG	1020
Db	1376	CTCGACACACCTCCTGATGTGGACGGCAAGTCTGTCTCAAACCTTCTGGACCCAGAAAAG	1435
Qy	1021	CCAGGTAACAGGTTTCGAACAAACAAGAAGGCCAAAATTTGGCGTGATACATTCTTAGTG	1080
Db	1436	CCAGGTAACAGGTTTCGAACAAACAAGAAGGCCAAAATTTGGCGTGATACATTCTTAGTG	1495
Qy	1081	GAAAGAGGCAAATTTCTACGTAAGAAGGAAGAATCCAGCAAGAATATCCAACAGTCAAAT	1140
Db	1496	GAAAGAGGCAAATTTCTACGTAAGAAGGAAGAATCCAGCAAGAATATCCAACAGTCAAAT	1555
Qy	1141	CACTTGCCCCAAATATGAACGGGTCAAAGAAGTATGCCAGCAGGCCAGGTACCAGACAGCC	1200
Db	1556	CACTTGCCCCAAATATGAACGGGTCAAAGAAGTATGCCAGCAGGCCAGGTACCAGACAGCC	1615
Qy	1201	TGTGAACAACCGGGGCAGAAGTGGCAATGCATTGAGGATACATCTGGCAAGCTTCGAATT	1260
Db	1616	TGTGAACAACCGGGGCAGAAGTGGCAATGCATTGAGGATACATCTGGCAAGCTTCGAATT	1675
Qy	1261	CACAAGTGTAAGGACCCAGTGACCTGCTCACAGTCCGGCAGAGCACGCGGAACCTCTAC	1320
Db	1676	CACAAGTGTAAGGACCCAGTGACCTGCTCACAGTCCGGCAGAGCACGCGGAACCTCTAC	1735
Qy	1321	GCTCGCGGCTTCCATGACAAAGACAAAGAGTGCAGTTGTAGGGAGTCTGGTTACCGTGCC	1380
Db	1736	GCTCGCGGCTTCCATGACAAAGACAAAGAGTGCAGTTGTAGGGAGTCTGGTTACCGTGCC	1795
Qy	1381	AGCAGAAGCCAAAGAAAGAGTCAACGGCAATTCTTGAGAAACCAGGGGACTCCAAAGTAC	1440
Db	1796	AGCAGAAGCCAAAGAAAGAGTCAACGGCAATTCTTGAGAAACCAGGGGACTCCAAAGTAC	1855
Qy	1441	AAGCCCAGATTTGTCCATACTCGGCAGACACGTTCCCTTGTCGGTCCAATTTGAAGGTGAA	1500
Db	1856	AAGCCCAGATTTGTCCATACTCGGCAGACACGTTCCCTTGTCGGTCCAATTTGAAGGTGAA	1915
Qy	1501	ATATATGACATAAATCTGGAAGAAGAAGAAGATTGCAAGTGTTGCAACCAAGAAACATT	1560
Db	1916	ATATATGACATAAATCTGGAAGAAGAAGAAGATTGCAAGTGTTGCAACCAAGAAACATT	1975
Qy	1561	GCTAAGCGTCATGATGAAGGCCACAAGGGGCCAAGAGATCTCCAGGCTTCCAGTGGTGGC	1620
Db	1976	GCTAAGCGTCATGATGAAGGCCACAAGGGGCCAAGAGATCTCCAGGCTTCCAGTGGTGGC	2035
Qy	1621	AACAGGGGCAGGATGCTGGCAGATAGCAGCAACGCCGTGGGCCCACCTACCACTGTCCGA	1680
Db	2036	AACAGGGGCAGGATGCTGGCAGATAGCAGCAACGCCGTGGGCCCACCTACCACTGTCCGA	2095
Qy	1681	GTGACACACAAGTGTTTTATTCTTCCCAATGACTCTATCCATTGTGAGAGAGAACTGTAC	1740
Db	2096	GTGACACACAAGTGTTTTATTCTTCCCAATGACTCTATCCATTGTGAGAGAGAACTGTAC	2155

Qy	1741	CAATCGGCCAGAGCGTGGAAGGACCATAAGGCATACATTGACAAAGAGATTGAAGCTCTG	1800
Db	2156	CAATCGGCCAGAGCGTGGAAGGACCATAAGGCATACATTGACAAAGAGATTGAAGCTCTG	2215
Qy	1801	CAAGATAAAATTAAGAATTTAAGAGAAGTGAGAGGACATCTGAAGAGAAGGAAGCCTGAG	1860
Db	2216	CAAGATAAAATTAAGAATTTAAGAGAAGTGAGAGGACATCTGAAGAGAAGGAAGCCTGAG	2275
Qy	1861	GAATGTAGCTGCAGTAAACAAAGCTATTACAATAAAGAGAAAGGTGTAAAAAAGCAAGAG	1920
Db	2276	GAATGTAGCTGCAGTAAACAAAGCTATTACAATAAAGAGAAAGGTGTAAAAAAGCAAGAG	2335
Qy	1921	AAATTTAAAGAGCCATCTTCACCCATTCAAGGAGGCTGCTCAGGAAGTAGATAGCAAACCTG	1980
Db	2336	AAATTTAAAGAGCCATCTTCACCCATTCAAGGAGGCTGCTCAGGAAGTAGATAGCAAACCTG	2395
Qy	1981	CAACTTTTCAAGGAGAAACAACCGTAGGAGGAAGAAGGAGAGGAAGGAGAAGAGACGGCAG	2040
Db	2396	CAACTTTTCAAGGAGAAACAACCGTAGGAGGAAGAAGGAGAGGAAGGAGAAGAGACGGCAG	2455
Qy	2041	AGGAAGGGGGAAGAGTGCAGCCTGCCTGGCCTCACTTGCTTCACGCATGACAACAACCAC	2100
Db	2456	AGGAAGGGGGAAGAGTGCAGCCTGCCTGGCCTCACTTGCTTCACGCATGACAACAACCAC	2515
Qy	2101	TGGCAGACAGCCCCGTTCTGGAACCTGGGATCTTTCTGTGCTTGACAGAGTTCTAACAAT	2160
Db	2516	TGGCAGACAGCCCCGTTCTGGAACCTGGGATCTTTCTGTGCTTGACAGAGTTCTAACAAT	2575
Qy	2161	AACACCTACTGGTGTTTGCGTACAGTTAATGAGACGCATAATTTTCTTTTCTGTGAGTTT	2220
Db	256	AACACCTACTGGTGTTTGCGTACAGTTAATGAGACGCATAATTTTCTTTTCTGTGAGTTT	2635
Qy	2221	GCTACTGGCTTTTTTGAGTATTTTGATATGAATACAGATCCTTATCAGCTCACAAATACA	2280
Db	2636	GCTACTGGCTTTTTTGAGTATTTTGATATGAATACAGATCCTTATCAGCTCACAAATACA	2695
Qy	2281	GTGCACACGGTAGAACGAGGCATTTTGAATCAGCTACACGTACAACCTAATGGAGCTCAGA	2340
Db	2696	GTGCACACGGTAGAACGAGGCATTTTGAATCAGCTACACGTACAACCTAATGGAGCTCAGA	2755
Qy	2341	AGCTGTCAAGGATATAAGCAGTGCAACCCAAGACCTAAGAATCTTGATGTTGGAAATAAA	2400
Db	2756	AGCTGTCAAGGATATAAGCAGTGCAACCCAAGACCTAAGAATCTTGATGTTGGAAATAAA	2815
Qy	2401	GATGGAGGAAGCTATGACCTACACAGAGGACAGTTATGGGATGGATGGGAAGGTTAATCA	2460
Db	2816	GATGGAGGAAGCTATGACCTACACAGAGGACAGTTATGGGATGGATGGGAAGGTTAATCA	2875
Qy	2461	GCCCCGTCTCACTGCAGACATCAACTGGCAAGGCCAGAGGAGCTACACAGTGTGAATGA	2520
Db	2876	GCCCCGTCTCACTGCAGACATCAACTGGCAAGGCCAGAGGAGCTACACAGTGTGAATGA	2935
Qy	2521	AAACATCTATGAGTACAGACAAAACCTACAGACTTAGTCTGGTGGACTGGACTAATTACTT	2580
Db	2936	AAACATCTATGAGTACAGACAAAACCTACAGACTTAGTCTGGTGGACTGGACTAATTACTT	2995
Qy	2581	GAAGGATTTAGATAGAGTATTTGCACTGCTGAAGAGTCACTATGAGCAAAATAAAACAAA	2640
Db	2996	GAAGGATTTAGATAGAGTATTTGCACTGCTGAAGAGTCACTATGAGCAAAATAAAACAAA	3055

QY 2641 TAAGACTCAAAGTCTGCTCAAAGTGACGGGTTCTTGGTTGTCTCTGCTGAGCACGCTGTGTC 2700  
 |||  
 Db 3056 TAAGACTCAAAGTCTGCTCAAAGTGACGGGTTCTTGGTTGTCTCTGCTGAGCACGCTGTGTC 3115

QY 2701 AATGGAGATGGCCTCTGCTGACTCAGATGAAGACCCAAGGCATAAGGTTGGGAAAACACC 2760  
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 Db 3116 AATGGAGATGGCCTCTGCTGACTCAGATGAAGACCCAAGGCATAAGGTTGGGAAAACACC 3175

QY 2761 TCATTTGACCTTGCCAGCTGACCTTCAAACCCCTGCATTGAACCGACCAACATTAAGTCC 2820  
 |||  
 Db 3176 TCATTTGACCTTGCCAGCTGACCTTCAAACCCCTGCATTGAACCGACCAACATTAAGTCC 3235

QY 2821 AGAGAGTAAACTTGAATGGAATAACGACATTCCAGAAGTTAATCATTTGAATTCTGAACA 2880  
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 Db 3236 AGAGAGTAAACTTGAATGGAATAACGACATTCCAGAAGTTAATCATTTGAATTCTGAACA 3295

QY 2881 CTGGAGAAAAACCGAAAAATGGACGGGGCATGAAGAGACTAATCATCTGGAAACCGATTT 2940  
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 Db 3296 CTGGAGAAAAACCGAAAAATGGACGGGGCATGAAGAGACTAATCATCTGGAAACCGATTT 3355

QY 2941 CAGTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCCAGCCCCAGGCTGCAGCCCATTTCG 3000  
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 Db 3356 CAGTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCCAGCCCCAGGCTGCAGCCCATTTCG 3415

QY 3001 CAGGCACCCGAAAGAAGTTCCTTCCAGTATGGTGGTCTTGAAAGGACATTTTGAAGATCA 3060  
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 Db 3416 CAGGCACCCGAAAGAAGTTCCTTCCAGTATGGTGGTCTTGAAAGGACATTTTGAAGATCA 3475

QY 3061 ACTATATCTTCTGTGCATTCCGATGGAATTTAGTTTCATCAGATGTTACCATTGGCCAC 3120  
 |||  
 Db 3476 ACTATATCTTCTGTGCATTCCGATGGAATTTAGTTTCATCAGATGTTACCATTGGCCAC 3535

QY 3121 CGCAGAACACCGAAGTAATTCCAGCATAGCGGGGAAGATGTTGACCAAGGTGGAGAAGAA 3180  
 |||  
 Db 3536 CGCAGAACACCGAAGTAATTCCAGCATAGCGGGGAAGATGTTGACCAAGGTGGAGAAGAA 3595

QY 3181 TCACGAAAAGGAGAAGTCACAGCACCTAGAAGGCAGCGCTCTCTTCACTCTCCTCTGA 3240  
 |||  
 Db 3596 TCACGAAAAGGAGAAGTCACAGCACCTAGAAGGCAGCGCTCTCTTCACTCTCCTCTGA 3655

QY 3241 TTAGATGAAACTGTTACCTTACCCTAAACACAGTATTTCTTTTAACTTTTTTATTTGTA 3300  
 |||  
 Db 3656 TTAGATGAAACTGTTACCTTACCCTAAACACAGTATTTCTTTTAACTTTTTTATTTGTA 715

QY 3301 AACTAATAAAGGTAATCACAGCCACCAACATTCCAAGCTACCCTGGGTACCTTTGTGCAG 3360  
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 Db 3716 AACTAATAAAGGTAATCACAGCCACCAACATTCCAAGCTACCCTGGGTACCTTTGTGCAG 3775

QY 3361 TAGAAGCTAGTGAGCATGTGAGCAAGCGGTGTGCACACGGAGACTCATCGTTATAATTTA 3420  
 |||  
 Db 3776 TAGAAGCTAGTGAGCATGTGAGCAAGCGGTGTGCACACGGAGACTCATCGTTATAATTTA 3835

QY 3421 CTATCTGCCAAGAGTAGAAAGAAAGGCTGGGGATATTTGGGTTGGCTTTGGTTTTGATTTT 3480  
 |||  
 Db 3836 CTATCTGCCAAGAGTAGAAAGAAAGGCTGGGGATATTTGGGTTGGCTTTGGTTTTGATTTT 3895

QY 3481 TTGCTTGTTTGTGTTTGTGTTTGTACTAAAACAGTATTATCTTTTGAATATCGTAGGGACATA 3540  
 |||  
 Db 3896 TTGCTTGTTTGTGTTTGTGTTTGTACTAAAACAGTATTATCTTTTGAATATCGTAGGGACATA 3955

QY	3541	AGTATATACATGTTATCCAATCAAGATGGCTAGAAATGGTGCCTTTCTGAGTGTCTAAAAC	3600
Db	3956	AGTATATACATGTTATCCAATCAAGATGGCTAGAAATGGTGCCTTTCTGAGTGTCTAAAAC	4015
QY	3601	TTGACACCCCTGGTAAATCTTTCAACACACTTCCACTGCCTGCGTAATGAAGTTTTGATT	3660
Db	4016	TTGACACCCCTGGTAAATCTTTCAACACACTTCCACTGCCTGCGTAATGAAGTTTTGATT	4075
QY	3661	CATTTTAAACCACTGGAATTTTTCAATGCCGTCATTTTCAGTTAGATGATTTTGCACCTT	3720
Db	4076	CATTTTAAACCACTGGAATTTTTCAATGCCGTCATTTTCAGTTAGATGATTTTGCACCTT	4135
QY	3721	GAGATTAAATGCCATGTCTATTTGATTAGTCTTATTTTTTTATTTTTACAGGCTTATCA	3780
Db	4136	GAGATTAAATGCCATGTCTATTTGATTAGTCTTATTTTTTTATTTTTACAGGCTTATCA	4195
QY	3781	GTCTCACTGTTGGCTGTCATTGTGACAAAGTCAAATAAACCCCCAAGGACGACACACAGT	3840
Db	4196	GTCTCACTGTTGGCTGTCATTGTGACAAAGTCAAATAAACCCCCAAGGACGACACACAGT	4255
QY	3841	ATGGATCACATATTGTTGACATTAAGCTTTTGCCAGAAAATGTTGCATGTGTTTTACCT	3900
Db	4256	ATGGATCACATATTGTTTGACATTAAGCTTTTGCCAGAAAATGTTGCATGTGTTTTACCT	4315
QY	3901	CGACTTGCTAAAATCGATTAGCAGAAAGGCATGGCTAATAATGTTGGTGGTGAAAATAAA	3960
Db	4316	CGACTTGCTAAAATCGATTAGCAGAAAGGCATGGCTAATAATGTTGGTGGTGAAAATAAA	4375
QY	3961	TAAATAAGTAAACAAAATGAAGATTGCCTGCTCTCTCTGTGCCTAGCCTCAAAGCGTTCA	4020
Db	4376	TAAATAAGTAAACAAAAWRAARAWWGCTGCTCTCTCTGTGCCTAGCCTCAAAGCGTTCA	4435
QY	4021	TCATACATCATACCTTTAAGATTGCTATATTTTGGGTTATTTTCTTGACAGGAGAAAAAG	4080
Db	4436	TCATACATCATACCTTTAAGATTGCTATATTTTGGGTTATTTTCTTGACAGGAGAAAAAG	4495
QY	4081	ATCTAAAGATCTTTTATTTTCATCTTTTTTGGTTTTCTTGGCATGACTAAGAAGCTTAAA	4140
Db	4496	ATCTAAAGATCTTTTATTTTCATCTTTTTTGGTTTTCTTGGCATGACTAAGAAGCTTAAA	4555
QY	4141	TGTTGATAAAATATGACTAGTTTTGAATTTACACCAAGAACTTCTCAATAAAAGAAAATC	4200
Db	4556	TGTTGATAAAATATGACTAGTTTTGAATTTACACCAAGAACTTCTCAATAAAAGAAAATC	4615
QY	4201	ATGAATGCTCCACAATTTCAACATACCACAAGAGAAGTTAATTTCTTAACATTGTGTTCT	4260
Db	4616	ATGAATGCTCCACAATTTCAACATACCACAAGAGAAGTTAATTTCTTAACATTGTGTTCT	4675
QY	4261	ATGATTATTTGTAAGACCTTCACCAAGTTCTGATATCTTTTAAAGACATAGTTCAAAATT	4320
Db	4676	ATGATTATTTGTAAGACCTTCACCAAGTTCTGATATCTTTTAAAGACATAGTTCAAAATT	4735
QY	4321	GCTTTTGAAAATCTGTATTCTTGAAAATATCCTTGTTGTGTATTAGGTTTTTAAATACCA	4380
Db	4736	GCTTTTGAAAATCTGTATTCTTGAAAATATCCTTGTTGTGTATTAGGTTTTTAAATACCA	4795
QY	4381	GCTAAAGGATTACCTCACTGAGTCATCAGTACCCTCCTATTTCAGCTCCCCAAGATGATGT	4440
Db	4796	GCTAAAGGATTACCTCACTGAGTCATCAGTACCCTCCTATTTCAGCTCCCCAAGATGATGT	4855

QY	4441	GTTTTTGCTTACCCTAAGAGAGGTTTTCTTCTTATTTTGTAGATAATTCAAGTGCTTAGAT	4500
Db	4856	GTTTTTGCTTACCCTAAGAGAGGTTTTCTTCTTATTTTGTAGATAATTCAAGTGCTTAGAT	4915
QY	4501	AAATTATGTTTTCTTTAAGTGTTTATGGTAAACTCTTTTAAAGAAAATTTAATATGTTAT	4560
Db	4916	AAATTATGTTTTCTTTAAGTGTTTATGGTAAACTCTTTTAAAGAAAATTTAATATGTTAT	4975
QY	4561	AGCTGAATCTTTTTGGTAACTTTAAATCTTTATCATAGACTCTGTACATATGTTCAAATT	4620
Db	4976	AGCTGAATCTTTTTGGTAACTTTAAATCTTTATCATAGACTCTGTACATATGTTCAAATT	5035
QY	4621	AGCTGCTTGCCTGATGTGTGTATCATCGGTGGGATGACAGAACAAACATATTTATGATCA	4680
Db	5036	AGCTGCTTGCCTGATGTGTGTATCATCGGTGGGATGACAGAACAAACATATTTATGATCA	5095
QY	4681	TGAATAATGTGCTTTGTAAAAAGATTTCAAGTTATTAGGAAGCATACTCTGTTTTTTAAT	4740
Db	5096	TGAATAATGTGCTTTGTAAAAAGATTTCAAGTTATTAGGAAGCATACTCTGTTTTTTAAT	5155
QY	4741	CATGTATAATATTCCATGATACTTTTATAGAACAATTCTGGCTTCAGGAAAGTCTAGAAG	4800
Db	5156	CATGTATAATATTCCATGATACTTTTATAGAACAATTCTGGCTTCAGGAAAGTCTAGAAG	5215
QY	4801	CAATATTTCTTCAAATAAAAGGTGTTTAACTTT	4834
Db	5216	CAATATTTCTTCAAATAAAAGGTGTTTAACTTT	5249